

---

**Barry**

**Samuel Hinton**

**Oct 16, 2023**



**CONTENTS:**

<b>1</b>	<b>Installation</b>	<b>3</b>
<b>2</b>	<b>Authors</b>	<b>5</b>
<b>3</b>	<b>Issues</b>	<b>7</b>
<b>4</b>	<b>How to Use</b>	<b>9</b>
<b>5</b>	<b>Index</b>	<b>11</b>
5.1	Barry API . . . . .	11



Welcome to the online documentation for Barry.

Check out the [config file](#) for examples on how to use Barry.

Or read through the



## INSTALLATION

Barry requires the following dependencies:

```
numpy  
scipy  
matplotlib  
chainconsumer  
emcee  
dynesty  
pandas  
camb  
hankel  
pyyaml
```

You can install Barry either locally, or if you want to pip install it, run:

```
pip install barry
```





---

CHAPTER  
TWO

---

**AUTHORS**

- Samuel Hinton: [samuelreay@gmail.com](mailto:samuelreay@gmail.com)
- Cullan Howlett: [c.howlett@uq.edu.au](mailto:c.howlett@uq.edu.au)



## ISSUES

Please raise issues, bugs and feature requests [on the Github Issues Page](#).



## HOW TO USE

1. Ensure that you have a named conda environment of at least python 3.6.
2. Clone this project onto both your local computer and a cluster computer
3. Have all dependencies installed: `pip install -r requirements.txt`
4. Update `config.yml` to include the name of your environment for activation on the HPC
5. **Run any of the python files in `barry.config`.**
  1. If you run on your local computer (ie `python test.py`), it will run the first MCMC run only to verify it works.
  2. If you run on a cluster (checks for cluster if the OS is centos, let me know if yours isn't), it will create a slurm job script and send out all needed runs
  3. Once all jobs have finished, copy the output from the plots folder ie `barry.config.plots.mocks` to your local computer
  4. Run the same python script and it will load in the data and create the plots.

Check out the API below or browse the examples used to make the Barry paper. For any questions, flick me an email ([samuelreay@gmail.com](mailto:samuelreay@gmail.com)).



## **5.1 Barry API**